MAIL DAINE CHICELLED

SEQUENCE LISTING

<110> PHARMACEUTICAL, INC.

HIATT, ANDREW C. HEIN, MICH B. FITCHEN, JOHN H.

NOVEL EPITHELIAL TISSUE IMAGING AGENT

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<150> 09/005,167

<151> 1998-01-09

<150> 08/782,480

<151> 1997-01-10

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Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu
35 40 45

Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Pro Val Tyr His 50 55 60

Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp 65 70 75 80

Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser 85 90 95

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Ile Val Glu Arg Asn Val Arg Ile Ile Val Pro Leu Asn Ser Arg Glu 35 40 45

Asn Ile Ser Asp Pro Thr Ser Pro Met Arg Thr Lys Pro Val Tyr His 50 55 60

Leu Ser Asp Leu Cys Lys Lys Cys Asp Thr Thr Glu Val Glu Leu Glu 65 70 75 80

Asp Gln Val Val Thr Ala Ser Gln Ser Asn Ile Cys Asp Ser Asp Ala 85 90 95

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Ile Ser Asp Pro Thr Ser Pro Leu Arg Arg Asn Pro Val Tyr His Leu 50 55 60

Ser Asp Val Cys Lys Cys Asp Pro Val Glu Val Glu Leu Glu Asp 65 70 75 80

Gln Val Val Thr Ala Thr Gln Ser Asn Ile Cys Asn Glu Asp Asp Gly 85 90 95

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Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Glu Pro Lys Tyr Asn Leu 50 55 60

Ala Asn Leu Cys Lys Lys Cys Asp Pro Thr Glu Ile Glu Leu Asp Asn 65 70 75 80

Gln Val Phe Thr Ala Ser Gln Ser Asn Ile Cys Pro Asp Asp Tyr 85 90 95

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	· As	p Gln	Gly	Val	Pro	Gln	Ser	Cys	Arg	Asp 90	Tyr	Cys	Pro	Glu	Leu 95	Asp
	Arg	g Asn	Lys	Cys 100	-	Thr	Val	Leu	Val 105		Pro	Gly	Tyr	Thr 110		Glu
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	T CGT a Arg															96
	T ATA p Ile															144
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240

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55

70

65 .

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Asp	Asn	Gln	·Ile	Val 85		Ala	Thr	Gln	Ser 90	Asn	Ile	Cys	Asp	Glu 95	Asp	
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				ACC Thr												33
			100		0,70	501		105	nop	J	A311	БуЗ	110	·	1111	
GCC	GTG	GTT	CCG	CTC	GTG	TAT	GGT	GGA	GAG	ACA	AAA	ATG	GTG	GAA	ACT	3.8
Ala		Val					Gly					Met				
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GCC										TGA	ATTC					42
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~220	-															
		CDS														
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<222 <220	>	(1).	-feat	ture	of Aı	ctifi	lcial	l Sed	quenc	ce: N	Jucl€	eotio	de se	equer	nce o	f Core T
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TCA GAG GAC CCA AAT GAA GAT ATA GTC GAA CGT AAC ATC CGT ATC ATC Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile 35 40 45	96
GTC CCA CTG AAT AAC CGG GAG AAT ATC TCA GAT CCT ACA AGT CCG TTG Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu 50 55 60	144
CGC ACA CGC TTC GTA TAC CAC CTG TCA GAT CTG TGT AAG AAG TGT GAT Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp 65 70 75	192
CCA ACA GAG GTA GAG CTG GAC AAT CAG ATA GTC ACT GCG ACT CAA AGC Pro Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser 80 85 90	240

AAC ATT TGC GAT GAG GAC AGC GCT ACA GAA ACC TGC TAC TGA 282
Asn Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr *
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A TITUTO
ATTC 286
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ATA GTC ACT GCG ACT CAA AGC AAC ATT TGC GAT GAG GAC AGC GCT ACA 96
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T 61

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Asp	Ile	Val 35	Glu	Arg	Asn	Ile	Arg		Ile	Val	Pro	Leu 45	Asn	Asn	Arg		
Glu	Asn 50	Ile	Ser	Asp	Pro	Thr	Ser	Pro	Leu	Arg	Thr	Arg	Phe	Val	Tyr		
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Asp	Asn	Gln	Ile	Val 85	Thr	Ala	Thr	Gln	Ser 90	Asn	Ile	Cys	Asp	Glu 95	Asp	٠	
Ser	Ala	Thr	Glu 100	Thr	Cys	Ser	Thr	Tyr 105	Asp	Arg	Asn	Lys	Cys 110	Tyr	Thr		
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Leu

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Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile 25

Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu 40

Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp 55

Pro Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser 75 70

Asn Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr 85

<210> 24 <211> 35 <212> Protein

<213> Artificial Sequence

<220>

<221> misc-feature

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<400> 24 Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp Asn Gln 10

Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser Ala Thr 25

Leu Trp Thr 35

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60

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AGATCTTAGT AGGCATCGAG TCTCCTGGGT TTACTTCTAT ATCAGCTTGC ATTGTAGGCA 120	
TAGTAGCAGG GTGACTTATT GGCCCTCTTA TAGAGTCTAG GATGTTCAGG CAACGCGTGT 180	
GCGAAGCATA TGGTGGACAG TCTAGACACA TTCTTCACAC TAGGTTGTCT CCATCTCGAC 240	
CTGTTAGTCT ATCAGTGACG CTGAGTTTCG TTGTAAACGC TACTCCTGTC GCGATGTCTT 300	
TGGACGTCGT GGATGCTATC CTTGTTTACG ATGTGCCGGC ACCAAGGCGA GCACATACCA 360	
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of C2 fragment	
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, and the second	
GCAGGGTGAC TTATTGGCCC TCTTATAGAG TCTAGGATGT TCAGGCAACG CGTGTGCGAA 120	
GCATATGGTG GACAGTCTAG 140	
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1011011	our didition in intermedial C	. 31
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<213>	Altilitial Sequence	
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	miles Feebour	
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ACACAT"	TCTT CCTACTTCTC AGGCGATGTC TTTGGACGAC TTAA	44
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of T4 1	fragment	• •
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TAGAGT	CTAG GATGTTCAGG	CAACGCGTGT	GCGAAGCATA	A TGGTGGACAG	TCTAGACACA	180
TTCTTC	ACAC TAGGTTGTCT	CCATCTCGAC	CTGTTAGTC	r atcagtgacg	CTGAGTTTCG	240
TTGTAA	ACGC TACTCCTGTC	GCGATGTCTT	TGGACGATG	A CT		282
<210><211><211><212><213>	105	uence .				
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ACTCAA	AGCA ACATTTGCGA	TGAGGACAGC	GCTACACTT	T GGACG	·	105
<210><211><211><212><213>	35 65 DNA Artificial Seq	uence				·
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AGATC						. 65

<210><211><212><213>	36 206 DNA Artificial Sequence		
	. =	Sequence: Complementary nucleotide s	sequence
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GTTTTG!	ACGC CTAAGGGCCT TCATTGTGGG	AGAGTCACGC GATTATTTCC GACGACAAAA	120
CTACTG	TGCC ATGCCCCGCA AGGCACCACG	AAGATGGGGT TATGTTAACT GCAAGGCGGA	180
CTTCTTC	CTCA CGCTCGGCAT TCTTAA		206
			·
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<400>. As	37 sp Gln Glu Asp Glu Arg Ile 5	Val Leu Val Asp Asn Lys	
<210><211><211><212><213>	38 7 Protein Tobacco etch virus		
	misc-feature Peptide recognized by the	tobacco etch virus protease Nia	
<400> Gl	38 lu Asn Leu Tyr Phe Gln Ser 5		

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<210> 39
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<221> misc-feature
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from pro-cathepsin E
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    , 1
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signal from pMelBac	
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Met Lys Phe Leu Val Asn Val Ala Leu Phe Met Val Val Tyr Ile Ser	
40 45 50	
TAC ATC TAT GCG GAT CCG AGC TCG AGT GCT CTAGATCTGC AGCTGGTACC	98
Tyr Ile Tyr Ala Asp Pro Ser Ser Ala	
55 60	
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	101
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1 5 10 15	
Tyr Ile Tyr Ala Asp Pro Ser Ser Ala	
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	1 5 10 15	
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CIROAA	- CONTROL CONT	•
T .		61
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T		61
1		
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CIAGAA	DOTTOTACT CONTANDAND ADDAMATETT ELLOADETTO ADDOCADONT ANTOL	
		٠.,
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<210>	52	
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(222)	Description of Aftifficial Dequence. Origonaticolide 1.2val	
<400>	52	
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_		<i>~</i> 3
T		61
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	II CI.II	

	<210>	56	
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	1220	v vodava	
	<220>		
		ming fortune	
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	12227	bescription of Artificial Sequence. Origonaciostias 3.149	
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		•	
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	12137	Hittietat ocquemec	
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1000/	postar parameter and a management of the parameter and a management of the parameter and a management of the parameter and a p	
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~~+C10.	1011 HOLEGORION GONCHOCOCI MCHONNACCI GCIG	44

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CA		62
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~4.13/	ALCILICIAL DOGACIEC	
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GATCTG	TGTA AGAAGTCTGA TATCGATGAA GATTCCGCTA CAGAAACCTG CAGCACATG	59

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210		
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-2227	Telelipelie el messiona bogacion. Ossignia sociale so	
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<210>	79	
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	Description of Artificial Sequence: Oligonucleotide 16	
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AATTOA	ore during the control thought in the control in the control of th	00
ACCATA	73.0	69
ACCAIA		09
	·	
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	DIT THITTIES GOODIIIGGII IBGIILGGGGG GIRAGGGGG IIIGGGGGI	50
ጥጥጥጥርጥር	CTCT CCACCATACA C	81
111101	TOT CONCONTRON C	0 1

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C	ys Ala Ala Pro Lys Lys Lys Arg Lys Val	
1	5 10	

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G.	ln Ala Lys Lys Lys
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IACCCC	MAIN CANTIDACOT TECOCETOAN ONNONOTOCO NOCCOTANO	7,
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